

ABSTRACT

A method is disclosed for predicting the risk of the occurrence of granulocytopenia caused by paclitaxel therapy in a subject. The method of the present invention comprises identifying a genetic polymorphism in a gene isolated from the subject for five SNPs in CYP2C8 gene (IMS-JST111898 (SEQ ID NO: 1), IMS-JST105874 (SEQ ID NO: 2), IMS-JST082397 (SEQ ID NO: 3), IMS-JST071852 (SEQ ID NO: 4) and IMS-JST071853 (SEQ ID NO: 5)) and for five SNPs in BUB1b gene (IMS-JST074538 (SEQ ID NO: 6), IMS-JST079837 (SEQ ID NO: 7), IMS-JST044164 (SEQ ID NO: 8), IMS-JST 063023 (SEQ ID NO: 9) and IMS-JST042569 (SEQ ID NO: 10)). A kit comprising a reagent used in the method of the present invention is also disclosed.